

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/881,736A
Source: IFW/16
Date Processed by STIC: 12/20/04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/20/2004

PATENT APPLICATION: US/09/881,736A

TIME: 12:22:01

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\12202004\I881736A.raw

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4 <110> APPLICANT: Glotzer, Michael
5      Jantsch-Plunger, Verena
6      Romano, Alper
7      Mishima, Masanori
8      Kaitna, Susanne
10 <120> TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their
use in screening
11      methods
13 <130> FILE REFERENCE: 0652.2260001/EKS/AES
15 <140> CURRENT APPLICATION NUMBER: US 09/881,736A
16 <141> CURRENT FILING DATE: 2001-06-18
18 <150> PRIOR APPLICATION NUMBER: EP 00 112 880.0
19 <151> PRIOR FILING DATE: 2000-06-19
21 <150> PRIOR APPLICATION NUMBER: EP 01 110 554.1
22 <151> PRIOR FILING DATE: 2001-04-30
24 <150> PRIOR APPLICATION NUMBER: 60/241,231
25 <151> PRIOR FILING DATE: 2000-10-18
27 <150> PRIOR APPLICATION NUMBER: To be determined
28 <151> PRIOR FILING DATE: 2001-06-13
31 <160> NUMBER OF SEQ ID NOS: 8
33 <170> SOFTWARE: PatentIn Ver. 2.1
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 3050
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
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46 <220> FEATURE:
47 <221> NAME/KEY: CDS
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50 <220> FEATURE:
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59      Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu
60      1          5          10
62 cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157
63 Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln
64      15          20          25
66 ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205
67 Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln

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71 Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala
72          50          55          60
74 gag act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat 301
75 Glu Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn
76          65          70          75
78 cag gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc 349
79 Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys
80          80          85          90
82 gaa aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt 397
83 Glu Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys
84          95          100          105
86 gac aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg 445
87 Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu
88 110          115          120          125
90 gct ttt ctc aac aga ggc caa cca tcc agc agc aat gct ggg aac aaa 493
91 Ala Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys
92          130          135          140
94 aga cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc 541
95 Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser
96          145          150          155
98 ttt gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag 589
99 Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys
100          160          165          170
102 act ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag 637
103 Thr Phe Lys Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln
104          175          180          185
106 ttt gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc 685
107 Phe Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly
108 190          195          200          205
110 tct gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg 733
111 Ser Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val
112          210          215          220
114 act gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag 781
115 Thr Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu
116          225          230          235
118 act gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa 829
119 Thr Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln
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122 cct tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga 877
123 Pro Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg
124          255          260          265
126 act gag aca gac agt gtg ggc acg cca cag agt aat gga ggg atg cgc 925
127 Thr Glu Thr Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg
128 270          275          280          285
130 ctg cat gac ttt gtt tct aag acg gtt att aaa cct gaa tcc tgt gtt 973
131 Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val
132          290          295          300

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136				305					310					315			
138	gac	tgt	cgt	gtg	gtc	tct	cat	cca	gaa	tgt	cgg	gac	cgc	tgt	ccc	ctt	1069
139	Asp	Cys	Arg	Val	Val	Ser	His	Pro	Glu	Cys	Arg	Asp	Arg	Cys	Pro	Leu	
140			320					325					330				
142	ccc	tgc	att	cct	acc	ctg	ata	gga	aca	cct	gtc	aag	att	gga	gag	gga	1117
143	Pro	Cys	Ile	Pro	Thr	Leu	Ile	Gly	Thr	Pro	Val	Lys	Ile	Gly	Glu	Gly	
144		335					340					345					
146	atg	ctg	gca	gac	ttt	gtg	tcc	cag	act	tct	cca	atg	atc	ccc	tcc	att	1165
147	Met	Leu	Ala	Asp	Phe	Val	Ser	Gln	Thr	Ser	Pro	Met	Ile	Pro	Ser	Ile	
148	350				355					360					365		
150	gtt	gtg	cat	tgt	gta	aat	gag	att	gag	caa	aga	ggg	ctg	act	gag	aca	1213
151	Val	Val	His	Cys	Val	Asn	Glu	Ile	Glu	Gln	Arg	Gly	Leu	Thr	Glu	Thr	
152				370					375					380			
154	ggc	ctg	tat	agg	atc	tct	ggc	tgt	gac	cgc	aca	gta	aaa	gag	ctg	aaa	1261
155	Gly	Leu	Tyr	Arg	Ile	Ser	Gly	Cys	Asp	Arg	Thr	Val	Lys	Glu	Leu	Lys	
156				385					390					395			
158	gag	aaa	ttc	ctc	aga	gtg	aaa	act	gta	ccc	ctc	ctc	agc	aaa	gtg	gat	1309
159	Glu	Lys	Phe	Leu	Arg	Val	Lys	Thr	Val	Pro	Leu	Leu	Ser	Lys	Val	Asp	
160		400						405					410				
162	gat	atc	cat	gct	atc	tgt	agc	ctt	cta	aaa	gac	ttt	ctt	cga	aac	ctc	1357
163	Asp	Ile	His	Ala	Ile	Cys	Ser	Leu	Leu	Lys	Asp	Phe	Leu	Arg	Asn	Leu	
164		415				420					425						
166	aaa	gaa	cct	ctt	ctg	acc	ttt	cgc	ctt	aac	aga	gcc	ttt	atg	gaa	gca	1405
167	Lys	Glu	Pro	Leu	Leu	Thr	Phe	Arg	Leu	Asn	Arg	Ala	Phe	Met	Glu	Ala	
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171	Ala	Glu	Ile	Thr	Asp	Glu	Asp	Asn	Ser	Ile	Ala	Ala	Met	Tyr	Gln	Ala	
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174	gtt	ggg	gaa	ctg	ccc	cag	gcc	aac	agg	gac	aca	tta	gct	ttc	ctc	atg	1501
175	Val	Gly	Glu	Leu	Pro	Gln	Ala	Asn	Arg	Asp	Thr	Leu	Ala	Phe	Leu	Met	
176			465					470					475				
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203 Leu Leu Gly Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro
204      575      580      585
206 tca tct agt tcc ctg tca cag aga gtc cgt tcc acc ctc acc aag aac 1885
207 Ser Ser Ser Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn
208 590      595      600      605
210 act cct aga ttt ggg agc aaa agc aag tct gcc act aac cta gga cga 1933
211 Thr Pro Arg Phe Gly Ser Lys Ser Lys Ser Ala Thr Asn Leu Gly Arg
212      610      615      620
214 caa ggc aac ttt ttt gct tct cca atg ctc aag tga agtcacatct 1979
215 Gln Gly Asn Phe Phe Ala Ser Pro Met Leu Lys
216      625      630
218 gcctgttact tcccagcatt gactgactat aagaaaggac acatctgtac tctgctctgc 2039
220 agcctcctgt actcattact acttttagca ttctccaggc ttttactcaa gtttaattgt 2099
222 gcatgagggt tttattaaaa ctatatatat ctccccttcc ttctcctcaa gtcacataat 2159
224 atcagcactt tgtgctggtc attggttggga gcttttagat gagacatctt tccaggggta 2219
226 gaagggttag tatggaattg gttgtgattc tttttgggga aggggggttat tgttcctttg 2279
228 gcttaaagcc aaatgctgct catagaatga tctttctcta gtttcattta gaactgattt 2339
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236 gggatgcatt gaggacagaa ctagtgatgg gagtatgctg agctttgatt tggatgatta 2579
238 ggtctttaat agtggttagt ggcacaacct tgtaaagtgt aaagtacaac tcgtatttat 2639
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244 acttctaaag gtcaatatat catcctttgg catcccaact accaataaag agtaggctat 2819
246 aagggaagat tgtcaatatt ttgtggtaag aaaagctaca gtcatttttt ctttgcactt 2879
248 tggatgctga aatttttccc atggaacata gccacatcta gatagatgtg agctttttct 2939
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267      20      25      30
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270      35      40      45
272 His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu
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275 Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp
276 65      70      75      80
278 Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu
279      85      90      95

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288      130      135      140
290 Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys
291 145      150      155      160
293 Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys
294      165      170      175
296 Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp
297      180      185      190
299 Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val
300      195      200      205
302 Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro
303      210      215      220
305 Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro
306 225      230      235      240
308 Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn
309      245      250      255
311 Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr Glu Thr
312      260      265      270
314 Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp
315      275      280      285
317 Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys Gly
318      290      295      300
320 Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg
321 305      310      315      320
323 Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile
324      325      330      335
326 Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala
327      340      345      350
329 Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His
330      355      360      365
332 Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr
333      370      375      380
335 Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe
336 385      390      395      400
338 Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His
339      405      410      415
341 Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro
342      420      425      430
344 Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile
345      435      440      445
347 Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu
348      450      455      460
350 Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His Leu
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